



EXHIBIT B

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☐ 1: [P51993](#). Reports Alpha-(1,3)-fucos...[gi:1730136]

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LOCUS P51993 359 aa linear PRI 04-DEC-2007
DEFINITION Alpha-(1,3)-fucosyltransferase (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 6) (FucT-VI).
ACCESSION P51993
VERSION P51993.1 GI:1730136
DBSOURCE swissprot: locus FUT6_HUMAN, accession P51993;
 class: standard.
 created: Oct 1, 1996.
 sequence updated: Oct 1, 1996.
 annotation updated: Dec 4, 2007.
 xrefs: [M98825.1](#), [AAA99222.1](#), [L01698.1](#), [AAB03078.1](#), [U27333.1](#), [AAC50192.1](#), [U27334.1](#), [AAC50193.1](#), [U27335.1](#), [AAC50194.1](#), [U27336.1](#), [AAC50195.1](#), [U27331.1](#), [AAC50190.1](#), [U27332.1](#), [AAC50191.1](#), [U27337.1](#), [AAC50196.1](#), [A45156](#), [I39048](#), [I39049](#)
 xrefs (non-sequence databases): RefSeq:[NP_000141.1](#), RefSeq:[NP_001035791.1](#), UniGene:[Hs.631846](#), UniGene:[Hs.695240](#), Ensembl:[ENSG00000156413](#), GeneID:[2528](#), KEGG:[hsa:2528](#), H-InvDB:[HIX0014674](#), HGNC:[4017](#), MIM:[136836](#), PharmGKB:[PA28433](#), ArrayExpress:[P51993](#), CleanEx:[HS_FUT6](#), GermOnline:[ENSG00000156413](#), GO:[0005794](#), GO:[0046920](#), GO:[0042355](#), GO:[0006486](#), InterPro:[IPR001503](#), PANTHER:[PTHR11929](#), Pfam:[PF00852](#)
KEYWORDS Alternative splicing; Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Polymorphism; Signal-anchor; Transferase; Transmembrane.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 359)
AUTHORS Koszdin, K.L. and Bowen, B.R.
TITLE The cloning and expression of a human alpha-1,3 fucosyltransferase capable of forming the E-selectin ligand
JOURNAL Biochem. Biophys. Res. Commun. 187 (1), 152-157 (1992)
PUBMED [1520296](#)
REMARK NUCLEOTIDE SEQUENCE [MRNA].
REFERENCE 2 (residues 1 to 359)
AUTHORS Weston, B.W., Smith, P.L., Kelly, R.J. and Lowe, J.B.
TITLE Molecular cloning of a fourth member of a human alpha (1,3)fucosyltransferase gene family. Multiple homologous sequences that determine expression of the Lewis x, sialyl Lewis x, and difucosyl sialyl Lewis x epitopes

JOURNAL J. Biol. Chem. 267 (34), 24575-24584 (1992)
 PUBMED [1339443](#)
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 Erratum: [J Biol Chem 1993 Aug 25;268(24):18398]
 REFERENCE 3 (residues 1 to 359)
 AUTHORS Cameron,H.S., Szczepaniak,D. and Weston,B.W.
 TITLE Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in normal tissues. Alternative splicing, polyadenylation, and isoforms
 JOURNAL J. Biol. Chem. 270 (34), 20112-20122 (1995)
 PUBMED [7650030](#)
 REMARK NUCLEOTIDE SEQUENCE [MRNA].
 TISSUE=Kidney
 COMMENT On or before Jul 18, 2007 this sequence version replaced [gi:2134726](#), [gi:2134727](#), [gi:539596](#).
 [FUNCTION] Enzyme involved in the biosynthesis of the E-Selectin ligand, sialyl-Lewis X. Catalyzes the transfer of fucose from GDP-beta-fucose to alpha-2,3 sialylated substrates.
 [CATALYTIC ACTIVITY] GDP-beta-L-fucose + beta-D-galactosyl-(1->3)-N-acetyl-D-glucosaminyl-R = GDP + beta-D-galactosyl-(1->3)-(alpha-L-fucosyl-(1->4))-N-acetyl-beta-D-glucosaminyl-R.
 [PATHWAY] Protein modification; protein glycosylation.
 [SUBCELLULAR LOCATION] Golgi apparatus, Golgi stack membrane; Single-pass type II membrane protein. Note=Membrane-bound form in trans cisternae of Golgi.
 [ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=P51993-1; Sequence=Displayed; Name=2; IsoId=P51993-2; Sequence=VSP_001780.
 [TISSUE SPECIFICITY] Kidney, liver, colon, small intestine, bladder, uterus and salivary gland.
 [SIMILARITY] Belongs to the glycosyltransferase 10 family.
 [WEB RESOURCE] Name=GGDB; Note=GlycoGene database; URL=<http://ggdb.muse.aist.go.jp/GGDB/index.jsp>.
 FEATURES
 Location/Qualifiers
 source 1..359
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 gene 1..359
 /gene="FUT6"
 /note="synonym: FCT3A"
 Protein 1..359
 /gene="FUT6"
 /product="Alpha-(1,3)-fucosyltransferase"
 /EC_number="2.4.1.65"
 Region 1..359
 /gene="FUT6"
 /region_name="Mature chain"
 /experiment="experimental evidence, no additional details recorded"
 /note="Alpha-(1,3)-fucosyltransferase."
 /FTId=PRO_0000221110."
 Region 1..14
 /gene="FUT6"
 /region_name="Topological domain"
 /inference="non-experimental evidence, no additional details recorded"
 /note="Cytoplasmic (Potential)."
 Region 5..358
 /gene="FUT6"

```

/region_name="Glyco_transf_10"
/note="Glycosyltransferase family 10 (fucosyltransferase).
This family of Fucosyltransferases are the enzymes
transferring fucose from GDP-Fucose to GlcNAc in an
alpha,3 linkage. This family is know as
glycosyltransferase family 10; pfam00852"
/db_xref="CDD:85069"
Region 15..34
/gene="FUT6"
/region_name="Transmembrane region"
/inference="non-experimental evidence, no additional
details recorded"
/note="Signal-anchor for type II membrane protein
(Potential)."
```

Region 35..359

```

/gene="FUT6"
/region_name="Topological domain"
/inference="non-experimental evidence, no additional
details recorded"
/note="Lumenal (Potential)."
```

Site 46

```

/gene="FUT6"
/site_type="glycosylation"
/inference="non-experimental evidence, no additional
details recorded"
/note="N-linked (GlcNAc...) (Potential)."
```

Site 91

```

/gene="FUT6"
/site_type="glycosylation"
/inference="non-experimental evidence, no additional
details recorded"
/note="N-linked (GlcNAc...) (Potential)."
```

Region 124

```

/gene="FUT6"
/region_name="Variant"
/experiment="experimental evidence, no additional details
recorded"
/note="P -> S (in dbSNP:rs778805). /FTId=VAR_024463."
```

Site 153

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/gene="FUT6"
/site_type="glycosylation"
/inference="non-experimental evidence, no additional
details recorded"
/note="N-linked (GlcNAc...) (Potential)."
```

Site 184

```

/gene="FUT6"
/site_type="glycosylation"
/inference="non-experimental evidence, no additional
details recorded"
/note="N-linked (GlcNAc...) (Potential)."
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Region 230

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/gene="FUT6"
/region_name="Variant"
/experiment="experimental evidence, no additional details
recorded"
/note="Q -> K (in dbSNP:rs364637). /FTId=VAR_024464."
```

Region 348..359

```

/gene="FUT6"
/region_name="Splicing variant"
/experiment="experimental evidence, no additional details
```

recorded"

/note="RYQTRGIAAWFT -> SSGGLIYLRTRLPEASPA (in isoform 2).

/FTId=VSP_001780."

ORIGIN

```
1 mdp1gppakpq wswrcclttl lfqllmavcf fsylrvsqdd ptvypngsrf pdstgtpahs
61 iplillwtwp fnkpialprc semvpgtadc nitadrkvyp qadavivvhr evmynpsaql
121 prsprrrggqr wiwfsmesps hcwqlkamdg yfnltmsyrs dsdiftpygw lepwsqgpah
181 pplnlsakte lvawavsnwg pnsarvryyq slqahlkvdv ygrshkplpq gtmmetlsry
241 kfylafensl hpdyitek1w rnaleawavp vvlgpsrsny erflppdafi hvddfqspkd
301 larylqeldk dharylsyfr wretlrprsf swalafckac wklqeesryq trgiaawft
```

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Aug 28 2007 16:53:42